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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53 (h))

Attorney Docket No. LEX-0091-USA

First Inventor C. Alexander Turner, Jr. et al.

Title Novel Human Notch Ligand Proteins and Polynucleotides

Express Mail label No. EL672756285US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

1 Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)

2 Applicant claims small entity status.
See 37 CFR 1.27.

3 Specification *[Total Pages* 26 *]*
(preferred arrangement set forth below)

- Descriptive title of the Invention
- Cross Reference to Related Applications
- Statement Regarding Fed sponsored R & D
- Reference to sequence listing, a table, or a computer program listing appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the drawings (if filed)
- Detailed Description
- Claim(s)
- Abstract of the disclosure

4 Drawing(s) (35 U.S.C. 113) *[Total Sheets*]

5 Oath or Declaration-unexecuted *[Total Pages* 2 *]*
a. Newly executed (original or copy)

b. Copy from a prior application (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)

i. **DELETION OF INVENTOR(S)**
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

6 Application Data Sheet See 37 CFR 1.76

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

7. CD-ROM or CD-R in duplicate, large table or Computer Program (Appendix)

8. Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)

a. Computer Readable Form (CRF)

b. Specification Sequence Listing on:

i. CD-ROM or CD-R (2 copies); or

i. paper

c. Statements verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

9. Assignment Papers (cover sheet & document(s))

10. 37 CFR 3.73(b) Statement
(when there is an assignee) Power of Attorney

11. English Translation Document (if applicable)

12. Information Disclosure Statement (IDS)/PTO-1449 Copies of IDS Citations

13. Preliminary Amendment

14. Return Receipt Postcard (MPEP 503)
(Should be specifically itemized)

15. Certified Copy of Priority Document(s)
(if foreign priority is claimed)

16. Other.

17. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in a preliminary amendment, or in an Application Data Sheet under 37 CFR 1.76:

Continuation Divisional Continuation-in-part (CIP)

of prior application No.: _____

Prior application information: Examiner _____

Group/Art Unit: _____

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 5b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference.

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Signature		Date	November 16, 2000
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NOVEL HUMAN NOTCH LIGAND PROTEINS AND
POLYNUCLEOTIDES ENCODING THE SAME

The present application claims the benefit of U.S.

5 Provisional Application Number 60/165,959 which was filed on
November 17, 1999 and is herein incorporated by reference in its
entirety.

1. INTRODUCTION

The present invention relates to the discovery,

10 identification, and characterization of novel human
polynucleotides encoding proteins that share sequence similarity
with mammalian SEL-1 proteins. The invention encompasses the
described polynucleotides, host cell expression systems, the
encoded proteins, fusion proteins, polypeptides and peptides,
15 antibodies to the encoded proteins and peptides, and genetically
engineered animals that either lack or over express the disclosed
genes, antagonists and agonists of the proteins, and other
compounds that modulate the expression or activity of the proteins
encoded by the disclosed genes that can be used for diagnosis,
20 drug screening, clinical trial monitoring and the treatment of
physiological disorders.

2. BACKGROUND OF THE INVENTION

SEL-1 proteins are negative regulators of *Notch* family
receptors. *Notch* receptors and their associated signaling
25 pathways have been associated with development, apoptosis, neuron
growth and maintenance. Genetic alterations in *Notch* receptors
and their ligands have been associated with multiple human
processes and disorders such as diabetes, cancer (*inter alia*
pancreatic cancer and insulinomas), stroke, Alzheimer's and other
30 neurodegenerative diseases, cholesterol and fat metabolism (HMG
CoA reductase degradation), blood pressure abnormalities, Coronary

artery disease and immunity (Donoviel and Bernstein, WO 99/27088, incorporated by reference in its entirety).

3. SUMMARY OF THE INVENTION

5 The present invention relates to the discovery, identification, and characterization of nucleotides that encode novel human proteins, and the corresponding amino acid sequences of these proteins. The novel human proteins (NHPs) described for the first time herein share structural similarity with animal
10 *Notch* ligands, and particularly SEL-1. As such, the novel *Notch* ligand proteins represent new members of the *Notch* ligand family, a family that has a range of homologues and orthologs that transcend phyla and species.

The novel human nucleic acid sequences described herein, 15 encode proteins/open reading frames (ORFs) of 689, 688, 590, 418, 499, 576, and 575 amino acids in length (see SEQ ID NOS: 2, 4, 6, 8, 10, 12, and 14 respectively).

The invention also encompasses agonists and antagonists of the described NHPs, including small molecules, large molecules, 20 mutant NHPs, or portions thereof that compete with native NHP, peptides, and antibodies, as well as nucleotide sequences that can be used to inhibit the expression of the described NHPs (e.g., antisense and ribozyme molecules, and gene or regulatory sequence replacement constructs) or to enhance the expression of the 25 described NHP sequences (e.g., expression constructs that place the described sequence under the control of a strong promoter system), and transgenic animals that express a NHP transgene, or "knock-outs" (which can be conditional) that do not express a functional NHP.

30 Further, the present invention also relates to processes for identifying compounds that modulate, i.e., act as agonists or antagonists, of NHP expression and/or NHP activity that utilize purified preparations of the described NHPs and/or NHP product, or

cells expressing the same. Such compounds can be used as therapeutic agents for the treatment of any of a wide variety of symptoms associated with biological disorders, including, but not limited to, diabetes, heart disease and cancer.

5

4. DESCRIPTION OF THE SEQUENCE LISTING AND FIGURES

The Sequence Listing provides the sequences of the NHP ORFs encoding the described NHP amino acid sequences.

10 5. DETAILED DESCRIPTION OF THE INVENTION

The NHPs, described for the first time herein, are novel proteins that are expressed in, *inter alia*, human testis cells and gene trapped human cell lines. The present invention encompasses the nucleotides presented in the Sequence Listing, host cells expressing such nucleotides, the expression products of such nucleotides, and: (a) nucleotides that encode mammalian homologs of the described sequences, including the specifically described NHPs, and the NHP products; (b) nucleotides that encode one or more portions of the NHPs that correspond to functional domains, and the polypeptide products specified by such nucleotide sequences, including but not limited to the novel regions of any active domain(s); (c) isolated nucleotides that encode mutant versions, engineered or naturally occurring, of the described NHPs in which all or a part of at least one domain is deleted or altered, and the polypeptide products specified by such nucleotide sequences, including but not limited to soluble proteins and peptides in which all or a portion of the signal sequence is deleted; (d) nucleotides that encode chimeric fusion proteins containing all or a portion of a coding region of an NHP, or one of its domains (e.g., a receptor or ligand binding domain, accessory protein/self-association domain, etc.) fused to another peptide or polypeptide; or (e) therapeutic or diagnostic derivatives of the described polynucleotides such as

oligonucleotides, antisense polynucleotides, ribozymes, dsRNA, or gene therapy constructs comprising a sequence first disclosed in the Sequence Listing. As discussed above, the present invention includes: (a) the human DNA sequences presented in the Sequence Listing (and vectors comprising the same) and additionally contemplates any nucleotide sequence encoding a contiguous NHP open reading frame (ORF) that hybridizes to a complement of a DNA sequence presented in the Sequence Listing under highly stringent conditions, e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. et al., eds., 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3) and encodes a functionally equivalent gene product. Additionally contemplated are any nucleotide sequences that hybridize to the complement of the DNA sequence that encode and express an amino acid sequence presented in the Sequence Listing under moderately stringent conditions, e.g., washing in 0.2xSSC/0.1% SDS at 42°C (Ausubel et al., 1989, *supra*), yet still encode a functionally equivalent NHP product. Functional equivalents of a NHP include naturally occurring NHPs present in other species and mutant NHPs whether naturally occurring or engineered (by site directed mutagenesis, gene shuffling, directed evolution as described in, for example, U.S. Patent No. 5,837,458). The invention also includes degenerate nucleic acid variants of the disclosed NHP polynucleotide sequences.

Additionally contemplated are polynucleotides encoding NHP ORFs, or their functional equivalents, encoded by polynucleotide sequences that are about 99, 95, 90, or about 85 percent similar or identical to corresponding regions of the nucleotide sequences of the Sequence Listing (as measured by BLAST sequence comparison analysis using, for example, the GCG sequence analysis package using standard default settings).

The invention also includes nucleic acid molecules, preferably DNA molecules, that hybridize to, and are therefore the complements of, the described NHP nucleotide sequences. Such hybridization conditions may be highly stringent or less highly 5 stringent, as described above. In instances where the nucleic acid molecules are deoxyoligonucleotides ("DNA oligos"), such molecules are generally about 16 to about 100 bases long, or about 20 to about 80, or about 34 to about 45 bases long, or any variation or combination of sizes represented therein that 10 incorporate a contiguous region of sequence first disclosed in the Sequence Listing. Such oligonucleotides can be used in conjunction with the polymerase chain reaction (PCR) to screen libraries, isolate clones, and prepare cloning and sequencing templates, etc.

15 Alternatively, such NHP oligonucleotides can be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high-throughput "chip" format). Additionally, a series of the described NHP oligonucleotide sequences, or the complements 20 thereof, can be used to represent all or a portion of the described NHP sequences. The oligonucleotides, typically between about 16 to about 40 (or any whole number within the stated range) nucleotides in length may partially overlap each other and/or the NHP sequence may be represented using oligonucleotides that do not 25 overlap. Accordingly, the described NHP polynucleotide sequences shall typically comprise at least about two or three distinct oligonucleotide sequences of at least about 18, and preferably about 25, nucleotides in length that are each first disclosed in the described Sequence Listing. Such oligonucleotide sequences 30 may begin at any nucleotide present within a sequence in the Sequence Listing and proceed in either a sense (5'-to-3') orientation vis-a-vis the described sequence or in an antisense orientation.

For oligonucleotide probes, highly stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos). These nucleic acid molecules may encode or act as NHP gene antisense molecules, useful, for example, in NHP gene regulation (for and/or as antisense primers in amplification reactions of NHP nucleic acid sequences). With respect to NHP gene regulation, such techniques can be used to regulate biological functions. Further, such sequences may be used as part of ribozyme and/or triple helix sequences that are also useful for NHP gene regulation.

Inhibitory antisense or double stranded oligonucleotides can additionally comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiacytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide can also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide will comprise at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a 5 methylphosphonate, an alkyl phosphotriester, and a formacetal or any combination or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in 10 which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA 15 analogue (Inoue et al., 1987, FEBS Lett. 215:327-330). Alternatively, double stranded RNA can be used to disrupt the expression and function of a targeted NHP.

Oligonucleotides of the invention can be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, 20 Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides can be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), and methylphosphonate oligonucleotides can be prepared by use of controlled pore glass 25 polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

Low stringency conditions are well known to those of skill in the art, and will vary predictably depending on the specific organisms from which the library and the labeled sequences are derived. For guidance regarding such conditions see, for example, 30 Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual (and periodic updates thereof), Cold Springs Harbor Press, N.Y.; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y.

Alternatively, suitably labeled NHP nucleotide probes can be used to screen a human genomic library using appropriately stringent conditions or by PCR. The identification and characterization of human genomic clones is helpful for 5 identifying polymorphisms (including, but not limited to, nucleotide repeats, microsatellite alleles, single nucleotide polymorphisms, or coding single nucleotide polymorphisms), determining the genomic structure of a given locus/allele, and designing diagnostic tests. For example, sequences derived from 10 regions adjacent to the intron/exon boundaries of the human gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (e.g., splice acceptor and/or donor sites), etc., that can be used in diagnostics and pharmacogenomics.

15 Further, a NHP sequence homolog can be isolated from nucleic acid from an organism of interest by performing PCR using two degenerate or "wobble" oligonucleotide primer pools designed on the basis of amino acid sequences within the NHP products disclosed herein. The template for the reaction may be total RNA, 20 mRNA, and/or cDNA obtained by reverse transcription of mRNA prepared from human or non-human cell lines or tissue known or suspected to express an allele of a NHP gene.

The PCR product can be subcloned and sequenced to ensure that the amplified sequences represent the sequence of the desired NHP. 25 The PCR fragment can then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment can be labeled and used to screen a cDNA library, such as a bacteriophage cDNA library. Alternatively, the labeled fragment can be used to isolate genomic clones via the screening of a 30 genomic library.

PCR technology can also be used to isolate full length cDNA sequences. For example, RNA can be isolated, following standard procedures, from an appropriate cellular or tissue source (i.e.,

one known, or suspected, to express a NHP sequence, such as, for example, testis or pancreatic tissue). A reverse transcription (RT) reaction can be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for 5 the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" using a standard terminal transferase reaction, the hybrid may be digested with RNase H, and second strand synthesis may then be primed with a complementary primer. Thus, cDNA sequences upstream of the amplified fragment can be 10 isolated. For a review of cloning strategies that can be used, see e.g., Sambrook *et al.*, 1989, *supra*.

A cDNA encoding a mutant NHP sequence can be isolated, for example, by using PCR. In this case, the first cDNA strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA 15 isolated from tissue known or suspected to be expressed in an individual putatively carrying a mutant NHP allele, and by extending the new strand with reverse transcriptase. The second strand of the cDNA is then synthesized using an oligonucleotide that hybridizes specifically to the 5' end of the normal gene. 20 Using these two primers, the product is then amplified via PCR, optionally cloned into a suitable vector, and subjected to DNA sequence analysis through methods well known to those of skill in the art. By comparing the DNA sequence of the mutant NHP allele to that of a corresponding normal NHP allele, the mutation(s) 25 responsible for the loss or alteration of function of the mutant NHP gene product can be ascertained.

Alternatively, a genomic library can be constructed using DNA obtained from an individual suspected of or known to carry a mutant NHP allele (e.g., a person manifesting a NHP-associated 30 phenotype such as, for example, obesity, high blood pressure, an inflammatory disorder, etc.), or a cDNA library can be constructed using RNA from a tissue known, or suspected, to express a mutant NHP allele. A normal NHP gene, or any suitable fragment thereof,

can then be labeled and used as a probe to identify the corresponding mutant NHP allele in such libraries. Clones containing mutant NHP gene sequences can then be purified and subjected to sequence analysis according to methods well known to 5 those skilled in the art.

Additionally, an expression library can be constructed utilizing cDNA synthesized from, for example, RNA isolated from a tissue known, or suspected, to express a mutant NHP allele in an individual suspected of or known to carry such a mutant allele. 10 In this manner, gene products made by the putatively mutant tissue can be expressed and screened using standard antibody screening techniques in conjunction with antibodies raised against a normal NHP product, as described below. (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, "Antibodies: A 15 Laboratory Manual", Cold Spring Harbor Press, Cold Spring Harbor.)

Additionally, screening can be accomplished by screening with labeled NHP fusion proteins, such as, for example, alkaline phosphatase-NHP or NHP-alkaline phosphatase fusion proteins. In cases where a NHP mutation results in an expressed gene product 20 with altered function (e.g., as a result of a missense or a frameshift mutation), polyclonal antibodies to a NHP are likely to cross-react with a corresponding mutant NHP gene product. Library clones detected via their reaction with such labeled antibodies can be purified and subjected to sequence analysis according to 25 methods well known in the art.

The invention also encompasses (a) DNA vectors that contain any of the foregoing NHP coding sequences and/or their complements (i.e., antisense); (b) DNA expression vectors that contain any of the foregoing NHP coding sequences operatively associated with a 30 regulatory element that directs the expression of the coding sequences (for example, baculo virus as described in U.S. Patent No. 5,869,336 herein incorporated by reference); (c) genetically engineered host cells that contain any of the foregoing NHP coding

sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell; and (d) genetically engineered host cells that express an endogenous NHP gene under the control of an exogenously introduced regulatory element (i.e., gene activation). As used herein, regulatory elements include, but are not limited to, inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression. Such regulatory elements include but are not limited to the human cytomegalovirus (hCMV) immediate early gene, regulatable, viral elements (particularly retroviral LTR promoters), the early or late promoters of SV40 adenovirus, the lac system, the trp system, the TAC system, the TRC system, the major operator and promoter regions of phage lambda, the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase (PGK), the promoters of acid phosphatase, and the promoters of the yeast α -mating factors.

Also encompassed by the present invention are novel protein constructs engineered in such a way that they facilitate transport of the NHP to the target site, to the desired organ, across the cell membrane and/or to the nucleus where the NHP can exert its function activity. This goal may be achieved by coupling of the NHP to a cytokine or other ligand that would direct the NHP to the target organ and facilitate receptor mediated transport across the membrane into the cytosol. Conjugation of NHPs to antibody molecules or their Fab fragments could be used to target cells bearing a particular epitope. Attaching the appropriate signal sequence to the NHP would also transport the NHP to the desired location within the cell. Alternatively targeting of NHP or its nucleic acid sequence might be achieved using liposome or lipid complex based delivery systems. Such technologies are described in U.S. Patents Nos. 4,594,595, 5,459,127, 5,948,767 and 6,110,490

and their respective disclosures which are herein incorporated by reference in their entirety.

The present invention also encompasses antibodies and anti-idiotypic antibodies (including Fab fragments), antagonists and 5 agonists of the NHP, as well as compounds or nucleotide constructs that inhibit expression of a NHP gene (transcription factor inhibitors, antisense and ribozyme molecules, or gene or regulatory sequence replacement constructs), or promote the expression of a NHP (e.g., expression constructs in which NHP 10 coding sequences are operatively associated with expression control elements such as promoters, promoter/enhancers, etc.).

The NHPs or NHP peptides, NHP fusion proteins, NHP nucleotide sequences, antibodies, antagonists and agonists can be useful for the detection of mutant NHPs or inappropriately expressed NHPs for 15 the diagnosis of disease. The NHP proteins or peptides, NHP fusion proteins, NHP nucleotide sequences, host cell expression systems, antibodies, antagonists, agonists and genetically engineered cells and animals can be used for screening for drugs (or high throughput screening of combinatorial libraries) 20 effective in the treatment of the symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. The use of engineered host cells and/or animals may offer an advantage in that such systems allow not only for the identification of compounds that bind to the endogenous receptor 25 for an NHP, but can also identify compounds that trigger NHP-mediated activities or pathways.

Finally, the NHP products can be used as therapeutics. For example, soluble derivatives such as NHP peptides/domains corresponding the NHPs, NHP fusion protein products (especially 30 NHP-Ig fusion proteins, *i.e.*, fusions of a NHP, or a domain of a NHP, to an IgFc), NHP antibodies and anti-idiotypic antibodies (including Fab fragments), antagonists or agonists (including compounds that modulate or act on downstream targets in a NHP-

mediated pathway) can be used to directly treat diseases or disorders. For instance, the administration of an effective amount of soluble NHP, or a NHP-IgFc fusion protein or an anti-idiotypic antibody (or its Fab) that mimics the NHP could activate 5 or effectively antagonize the endogenous NHP receptor. Soluble NHPs can also be modified by proteolytic cleavage to active peptide products (e.g., any novel peptide sequence initiating at any one of the amino acids presented in the Sequence Listing and ending at any downstream amino acid). Such products or peptides 10 can be further subject to modification such as the construction of NHP fusion proteins and/or can be derivatized by being combined with pharmaceutically acceptable agents such as, but not limited to, polyethylene glycol (PEG).

Nucleotide constructs encoding such NHP products can be used 15 to genetically engineer host cells to express such products *in vivo*; these genetically engineered cells function as "bioreactors" in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide constructs encoding functional NHPs, mutant NHPs, as well as 20 antisense and ribozyme molecules can also be used in "gene therapy" approaches for the modulation of NHP expression. Thus, the invention also encompasses pharmaceutical formulations and methods for treating or preventing biological disorders such as, but not limited to, Alzheimer's Disease, diabetes, cancer, 25 neurodegenerative diseases such as Parkinson's disease, stroke, vascular dementia, and conditions requiring modulation of fat and cholesterol metabolism such as coronary artery disease.

Various aspects of the invention are described in greater detail in the subsections below.

5.1 THE NHP SEQUENCES

The cDNA sequences and the corresponding deduced amino acid sequences of the described NHPs are presented in the Sequence Listing. The NHP nucleotides were obtained from human gene 5 trapped sequence tags and cDNA clones from a human testis cDNA library. A coding region single nucleotide polymorphism was observed during the generation of the described NHPs which consists of an A-to-G (or vice-versa) transition at base number 1,177 of, for example, SEQ ID NO:1 which results the presence of 10 an glu or a lys at corresponding amino acid position 393 of, for example, SEQ ID NO:2.

Because of the diverse activities that have been associated with *Notch* signaling pathways, *Notch* receptors, and their associated ligands and antagonists have been subject to intense 15 scientific scrutiny. For examples of how the described NHPs, or related *Notch* receptors can be produced, antagonized, used, processed, applied, and delivered, see, for example, U.S. Patent Nos. 5,786,158 and 5,780,300, and 5,856,441 the disclosures of which are hereby incorporated by reference in their entirety. 20 Given their structural relatedness to *Notch* ligands, the described NHPs are suitable for use and modification as contemplated for other *Notch* ligands and antagonists.

5.2 NHPS AND NHP POLYPEPTIDES

25 NHPs, polypeptides, peptide fragments, mutated, truncated, or deleted forms of the NHPs, and/or NHP fusion proteins can be prepared for a variety of uses. These uses include, but are not limited to, the generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene 30 products related to a NHP, as reagents in assays for screening for compounds that can be as pharmaceutical reagents useful in the therapeutic treatment of mental, biological, or medical disorders and disease.

The Sequence Listing discloses the amino acid sequences encoded by the described NHP encoding polynucleotides. The NHPs have initiator methionines in DNA sequence contexts consistent with a translation initiation site, and further incorporate a 5 hydrophobic leader sequence characteristic of secreted or membrane associated proteins.

The NHP amino acid sequences of the invention include the amino acid sequence presented in the Sequence Listing as well as analogues and derivatives thereof. Further, corresponding NHP 10 homologues from other species are encompassed by the invention. In fact, any NHP protein encoded by the NHP nucleotide sequences described above are within the scope of the invention, as are any novel polynucleotide sequences encoding all or any novel portion of an amino acid sequence presented in the Sequence Listing. The 15 degenerate nature of the genetic code is well known, and, accordingly, each amino acid presented in the Sequence Listing, is generically representative of the well known nucleic acid "triplet" codon, or in many cases codons, that can encode the amino acid. As such, as contemplated herein, the amino acid 20 sequences presented in the Sequence Listing, when taken together with the genetic code (see, for example, Table 4-1 at page 109 of "Molecular Cell Biology", 1986, J. Darnell *et al.* eds., Scientific American Books, New York, NY, herein incorporated by reference) are generically representative of all the various permutations and 25 combinations of nucleic acid sequences that can encode such amino acid sequences.

The invention also encompasses proteins that are functionally equivalent to the NHPs encoded by the presently described nucleotide sequences as judged by any of a number of criteria, 30 including, but not limited to, the ability to bind and cleave a substrate of a NHP, or the ability to effect an identical or complementary downstream pathway, or a change in cellular metabolism (e.g., proteolytic activity, ion flux, tyrosine

phosphorylation, etc.). Such functionally equivalent NHP proteins include, but are not limited to, additions or substitutions of amino acid residues within the amino acid sequence encoded by the NHP nucleotide sequences described above, but which result in a 5 silent change, thus producing a functionally equivalent gene product. Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include 10 alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) 15 amino acids include aspartic acid and glutamic acid.

A variety of host-expression vector systems can be used to express the NHP nucleotide sequences of the invention. Where, as in the present instance, the NHP peptide or polypeptide is thought to be a soluble or secreted molecule, the peptide or polypeptide 20 can be recovered from the culture media. Alternatively, if the described NHP is membrane associated, as characteristic of some *Notch* ligands, a soluble derivative can be engineered by deleting a transmembrane domain. Such expression systems also encompass engineered host cells that express a NHP, or functional 25 equivalent, *in situ*. Purification or enrichment of a NHP from such expression systems can be accomplished using appropriate detergents and lipid micelles and methods well known to those skilled in the art. However, such engineered host cells themselves may be used in situations where it is important not 30 only to retain the structural and functional characteristics of the NHP, but to assess biological activity, e.g., in drug screening assays.

The expression systems that can be used for purposes of the invention include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing NHP nucleotide sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing NHP nucleotide sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing NHP sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing NHP nucleotide sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the NHP product being expressed. For example, when a large quantity of such a protein is to be produced for the generation of pharmaceutical compositions of or containing NHP, or for raising antibodies to a NHP, vectors that direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which a NHP coding sequence may be ligated individually into the vector in frame with the *lacZ* coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the like. pGEX

vectors (Pharmacia or American Type Culture Collection) can also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by 5 adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The PGE_X vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear 10 polyhidrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. A NHP gene coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin 15 promoter). Successful insertion of NHP gene coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* 20 cells in which the inserted gene is expressed (e.g., see Smith et al., 1983, *J. Virol.* 46: 584; Smith, U.S. Patent No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems can be utilized. In cases where an adenovirus is used as an expression vector, the NHP nucleotide sequence of interest may 25 be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will 30 result in a recombinant virus that is viable and capable of expressing a NHP product in infected hosts (e.g., See Logan & Shenk, 1984, *Proc. Natl. Acad. Sci. USA* 81:3655-3659). Specific initiation signals may also be required for efficient translation

of inserted NHP nucleotide sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire NHP gene or cDNA, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression 5 vector, no additional translational control signals may be needed. However, in cases where only a portion of a NHP coding sequence is inserted, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of 10 the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, 15 transcription terminators, etc. (See Bittner *et al.*, 1987, Methods in Enzymol. 153:516-544).

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such 20 modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell 25 lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be 30 used. Such mammalian host cells include, but are not limited to, CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, and in particular, human cell lines.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the NHP sequences described above can be engineered. Rather than using expression vectors which contain 5 viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be 10 allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into 15 cell lines. This method may advantageously be used to engineer cell lines which express the NHP product. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the NHP product.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, *Cell* 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, *Proc. Natl. Acad. Sci. USA* 48:2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, *Cell* 22:817) genes can be employed in tk⁻, hprt⁻ or aprt⁻ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, *Natl. Acad. Sci. USA* 77:3567; O'Hare, et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al.,

1981, J. Mol. Biol. 150:1); and hygro, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30:147).

Alternatively, any fusion protein can be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-8976). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni^{2+} ·nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

15

5.3 ANTIBODIES TO NHP PRODUCTS

Antibodies that specifically recognize one or more epitopes of a NHP, or epitopes of conserved variants of a NHP, or peptide fragments of a NHP are also encompassed by the invention. Such antibodies include but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, $\text{F}(\text{ab}')_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above.

The antibodies of the invention may be used, for example, in the detection of NHP in a biological sample and may, therefore, be utilized as part of a diagnostic or prognostic technique whereby patients may be tested for abnormal amounts of NHP. Such antibodies may also be utilized in conjunction with, for example, compound screening schemes for the evaluation of the effect of test compounds on expression and/or activity of a NHP gene product. Additionally, such antibodies can be used in conjunction

gene therapy to, for example, evaluate the normal and/or engineered NHP-expressing cells prior to their introduction into the patient. Such antibodies may additionally be used as a method for the inhibition of abnormal NHP activity. Thus, such 5 antibodies may, therefore, be utilized as part of treatment methods.

For the production of antibodies, various host animals may be immunized by injection with the NHP, an NHP peptide (e.g., one corresponding the a functional domain of an NHP), truncated NHP 10 polypeptides (NHP in which one or more domains have been deleted), functional equivalents of the NHP or mutated variant of the NHP. Such host animals may include but are not limited to pigs, rabbits, mice, goats, and rats, to name but a few. Various 15 adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's adjuvant (complete and incomplete), mineral salts such as aluminum hydroxide or aluminum phosphate, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, and 20 potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*. Alternatively, the immune response could be enhanced by combination and or coupling with molecules such as keyhole limpet hemocyanin, tetanus toxoid, diphtheria toxoid, ovalbumin, cholera toxin 25 or fragments thereof. Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of the immunized animals.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, can be obtained by any 30 technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique of Kohler and Milstein, (1975, *Nature* 256:495-497; and U.S. Patent No. 4,376,110), the human B-

cell hybridoma technique (Kosbor *et al.*, 1983, *Immunology Today* 4:72; Cole *et al.*, 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole *et al.*, 1985, *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

5 Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated in vitro or in vivo. Production of high titers of mAbs in vivo makes this the presently preferred method of production.

10 In addition, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci.*, 81:6851-6855; Neuberger *et al.*, 1984, *Nature*, 312:604-608; Takeda *et al.*, 1985, *Nature*, 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity 15 together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region.

20 Such technologies are described in U.S. Patents Nos. 6,075,181 and 5,877,397 and their respective disclosures which are herein incorporated by reference in their entirety.

Alternatively, techniques described for the production of 25 single chain antibodies (U.S. Patent 4,946,778; Bird, 1988, *Science* 242:423-426; Huston *et al.*, 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward *et al.*, 1989, *Nature* 334:544-546) can be adapted to produce single chain antibodies against NHP gene products. Single chain antibodies are formed by linking the heavy 30 and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments

include, but are not limited to: the $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression 5 libraries may be constructed (Huse *et al.*, 1989, *Science*, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Antibodies to a NHP can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" a given NHP, using 10 techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, 1993, *FASEB J* 7(5):437-444; and Nissinoff, 1991, *J. Immunol.* 147(8):2429-2438). For example antibodies which bind to a NHP domain and competitively inhibit the binding of NHP to its cognate receptor can be used to generate anti-idiotypes that 15 "mimic" the NHP and, therefore, bind and activate or neutralize a receptor. Such anti-idiotypic antibodies or Fab fragments of such anti-idiotypes can be used in therapeutic regimens involving a NHP-mediated pathway.

The present invention is not to be limited in scope by the 20 specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will 25 become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims. All cited publications, patents, and patent applications are herein incorporated by reference in their entirety.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising at least 24 contiguous bases of nucleotide sequence first disclosed 5 in the NHP sequence described in SEQ ID NO:1.

2. An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a) encodes the amino acid sequence shown in SEQ ID 10 NO:2; and
(b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

15 3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.

4. An isolated nucleic acid molecule comprising a 20 nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.

5 An isolated nucleic acid molecule comprising a 25 nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.

6. An isolated nucleic acid molecule comprising a 30 nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.

ABSTRACT

Novel human polynucleotide and polypeptide sequences are disclosed that can be used in therapeutic, diagnostic, and pharmacogenomic applications.

PATENT APPLICATION**DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION**

ATTORNEY DOCKET NO. LEX-0091-USA

As a below named inventor, I hereby declare that:

My residence/post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Novel Human Notch Ligand Proteins and Polynucleotides Encoding the Same

the specification of which is attached hereto unless the following box is checked:

() was filed on _____ as US Application Serial No. or PCT International Application

Number _____ and was amended on _____ (if applicable).

I hereby state that I have reviewed and understood the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above. I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR 1.56.

Foreign Application(s) and/or Claim of Foreign Priority

I hereby claim foreign priority benefits under Title 35, United States Code Section 119 of any foreign application(s) for patent or inventor(s) certificate listed below and have also identified below any foreign application for patent or inventor(s) certificate having a filing date before that of the application on which priority is claimed:

COUNTRY	APPLICATION NUMBER	DATE FILED	PRIORITY CLAIMED UNDER 35 U.S.C. 119	
			YES:	NO:
			YES:	NO:

Provisional Application

I hereby claim the benefit under Title 35, United States Code Section 119(e) of any United States provisional application(s) listed below:

APPLICATION SERIAL NUMBER	FILING DATE
60/165,959	11/17/1999

U.S. Priority Claim

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

APPLICATION SERIAL NUMBER	FILING DATE	STATUS(patented/pending/abandoned)

POWER OF ATTORNEY:

As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) listed below to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Lance K. Ishimoto, Reg. No. 41866

Send Correspondence to: Lance K. Ishimoto Lexicon Genetics Incorporated 4000 Research Forest Drive The Woodlands, TX 77381	Direct Telephone Calls To: Lance K. Ishimoto (281) 362-6554
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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION (continued)

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<211> 688
<212> PRT
<213> *Homo sapiens*

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Arg Asn Val Thr Thr Gln Val Ser Val Asn Glu Ile Lys Gln Tyr Leu
  35          40          45
Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
  50          55          60
Glu Asn Leu Leu Glu Lys Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
  65          70          75          80
Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
  85          90          95
Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
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 Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
 145 150 155 160
 Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
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 Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
 180 185 190
 Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
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 Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
 210 215 220
 Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
 225 230 235 240
 Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
 245 250 255
 Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
 260 265 270
 Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
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 Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
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 Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
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 Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
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 Gln Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
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 Gly Asn Ala Ile Gly Leu His Gly Leu Leu Tyr Phe His Gly
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 Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
 385 390 395 400
 Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
 405 410 415
 Tyr Tyr Ser Gly Ser Gly Ile Trp Lys Asp Tyr Lys Leu Ala Phe Lys
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 Thr Ala Val Glu Leu Tyr Lys Gly Val Cys Glu Leu Gly His Trp Ala
 465 470 475 480
 Glu Lys Phe Leu Thr Ala Tyr Phe Ala Tyr Lys Asp Gly Asp Ile Asp
 485 490 495
 Ser Ser Leu Val Gln Tyr Ala Leu Leu Ala Glu Met Gly Tyr Glu Val
 500 505 510
 Ala Gln Ser Asn Ser Ala Phe Ile Leu Glu Ser Lys Lys Ala Asn Ile
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 Leu Glu Lys Glu Lys Met Tyr Pro Met Ala Leu Leu Leu Trp Asn Arg
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 Ala Ala Ile Gln Gly Asn Ala Phe Ala Arg Val Lys Ile Gly Asp Tyr

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His	Tyr	Gly	Tyr	Gly	Thr	Lys	Lys	Asp	Tyr	Gln	Thr	Ala	Ala	Thr	
565	570	575													
His	Tyr	Ser	Ile	Ala	Ala	Asn	Lys	Tyr	His	Asn	Ala	Gln	Ala	Met	Phe
580	585	590													
Asn	Leu	Ala	Tyr	Met	Tyr	Glu	His	Gly	Leu	Gly	Ile	Thr	Lys	Asp	Ile
595	600	605													
His	Leu	Ala	Arg	Arg	Leu	Tyr	Asp	Met	Ala	Ala	Gln	Thr	Ser	Pro	Asp
610	615	620													
Ala	His	Ile	Pro	Val	Leu	Phe	Ala	Val	Met	Lys	Leu	Glu	Thr	Thr	His
625	630	635	640												
Leu	Leu	Arg	Asp	Ile	Leu	Phe	Phe	Asn	Phe	Thr	Thr	Arg	Trp	Asn	Trp
645	650	655													
Leu	Lys	Leu	Asp	Asn	Thr	Ile	Gly	Pro	His	Trp	Asp	Leu	Phe	Val	Ile
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 <212> DNA
 <213> Homo sapiens

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gtgaacgaaa	tcaaacaata	tttatcacac	atattggAAC	aaagaacatc	tagtaatgt	180
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ggaattcaaa	ataaagatat	cttgaagaga	aataagaatc	atttacaaaa	gcaagcagag	300
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tctaaaagcc	aaaaacaaaa	agaagaagcc	tacctacttt	ttgccaaagc	agctgacatg	420
ggaaaacttga	aagctatgga	gaaaatggct	gacgcttgc	tatTTggaaa	ttttggcgtg	480
caaaatataa	cagcagctat	ccaattat	gagtccttgg	ctaaagaagg	atcatgtaaa	540
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aaggcactga	tatattacac	ctttggaa	gctggaggaa	acatgtatgc	ccagatgatt	660
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gattgggaca	tataccaata	ctataaattt	ttggcagaaa	gaggagatgt	tcagatacaa	900
gtctctctg	gacaattaca	tctaatttgc	aggaaaggtc	tagatcagga	ttactacaaa	960
gcattacact	acttcttaaa	ggcagcaaa	gccgggagtg	caaatgccc	ggcatttata	1020
ggaaaagatgt	atTTAGAGGG	gaatgctgg	gtgccc	ataacgctac	tgccttcaag	1080
tactttcca	tggcagccag	taaggcaat	gcaatggcc	ttcatgggt	ttgttctt	1140
tactttcatg	gaaaaggagt	tcccctgaat	tatgcccraag	cactttaata	ctttcagaaa	1200
gctgcggaaa	aagggtggcc	cgacgcacag	ttccagtt	gttcatgt	ctactctggc	1260
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gggcagcccc	tcgcattta	ttatctggcc	aagatgtatg	caacaggaa	aggagttagt	1380
agatcatgca	gaactgctgt	ggagctt	aaagggtgt	gtgaactagg	ccactggc	1440
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cagttatgcac	tgcttgcaga	aatgggtat	gaagtagctc	aaagcaattc	agcattcatt	1560
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ctatggaaatc	gagctgccc	tcaaggacat	tcacttggcc	agaagattgt	acgacatggc	1680
tgctcaaacg	agtccagatg	cccacatacc	tgtgctt	gccgtcatga	aactggaaac	1740
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<212> PRT
<213> Homo sapiens

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35 40 45
Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
50 55 60
Glu Asn Leu Leu Glu Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
65 70 75 80
Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
85 90 95
Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
100 105 110
Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
115 120 125
Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
130 135 140
Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
145 150 155 160
Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
165 170 175
Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
180 185 190
Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
195 200 205
Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
210 215 220
Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
225 230 235 240
Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
245 250 255
Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
260 265 270
Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
275 280 285
Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
290 295 300
Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
305 310 315 320
Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
325 330 335
Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
340 345 350
Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
355 360 365
Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
370 375 380
Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys

385	390	395	400
Ala	Ala	Glu	Lys
Gly	Trp	Pro	Asp
405	410	415	
Tyr	Tyr	Ser	Gly
Ile	Trp	Lys	Asp
420	425	430	
Tyr	Phe	Tyr	Leu
Ala	Ser	Gln	Ser
Gly	Gln	Pro	Leu
435	440	445	
Leu	Ala	Lys	Met
Tyr	Ala	Thr	Gly
450	455	460	
Thr	Ala	Val	Glu
Leu	Tyr	Lys	Gly
465	470	475	480
Glu	Lys	Phe	Leu
Thr	Ala	Tyr	Phe
485	490	495	
Ser	Ser	Leu	Val
Gln	Tyr	Ala	Leu
500	505	510	
Ala	Gln	Ser	Asn
Ser	Ala	Phe	Ile
515	520	525	
Leu	Glu	Lys	Glu
Lys	Met	Tyr	Pro
530	535	540	
Ala	Ala	Ile	Gln
Gly	His	Ser	Leu
545	550	555	560
Cys	Ser	Asn	Glu
Ser	Arg	Cys	Pro
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Glu	Thr	Gly	Asn
Tyr	Ala	Phe	Ala
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 <211> 1257
 <212> DNA
 <213> Homo sapiens

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ggaattcaaa	ataaaagatat	cttgaagaga	aataagaatc	atttacaaaaa	gcaaggcagag	300
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caaaatataa	cagcagctat	ccaattat	gagtccctgg	ctaaagaagg	atcatgtaaa	540
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<211> 418
<212> PRT
<213> Homo sapiens

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Arg Asn Val Thr Thr Gln Val Ser Val Asn Glu Ile Lys Gln Tyr Leu
35 40 45
Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
50 55 60
Glu Asn Leu Leu Glu Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
65 70 75 80
Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
85 90 95
Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
100 105 110
Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
115 120 125
Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
130 135 140
Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
145 150 155 160
Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
165 170 175
Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
180 185 190
Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
195 200 205
Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
210 215 220
Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
225 230 235 240
Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
245 250 255
Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
260 265 270
Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
275 280 285
Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
290 295 300
Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
305 310 315 320
Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
325 330 335
Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
340 345 350
Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
355 360 365
Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
370 375 380
Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
385 390 395 400

Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
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 <211> 1500
 <212> DNA
 <213> Homo sapiens

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 aaaaattttA cagatgaagg agaccAGCTA tttaAGATGG GcatcaAGGT tctccAGcAG 360
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 aaggcactGA tatattacac ctttggAAgt gctggaggAA acatgatgtc ccAGATGATT 660
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 gtggaaaaAG tgagactAAC gggAAAGACt gaaaATCTGA gttctAACAG tgagatTTG 840
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 gggcAGcccc tcGCCAttA ttatctGGC aagatgtAtG caacAGGAAC aggAGTAGtA 1380
 agatcatGcA gaactgctgt ggagAAAAGG ctaacattct tgaaaaAGAG aagatgtAtC 1440
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<210> 10
 <211> 499
 <212> PRT
 <213> Homo sapiens

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 Arg Asn Val Thr Thr Gln Val Ser Val Asn Glu Ile Lys Gln Tyr Leu
 35 40 45
 Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
 50 55 60
 Glu Asn Leu Leu Glu Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
 65 70 75 80
 Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
 85 90 95

Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
 100 105 110
 Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
 115 120 125
 Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
 130 135 140
 Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
 145 150 155 160
 Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
 165 170 175
 Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
 180 185 190
 Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
 195 200 205
 Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
 210 215 220
 Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
 225 230 235 240
 Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
 245 250 255
 Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
 260 265 270
 Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
 275 280 285
 Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
 290 295 300
 Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
 305 310 315 320
 Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
 325 330 335
 Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
 340 345 350
 Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
 355 360 365
 Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
 370 375 380
 Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
 385 390 395 400
 Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
 405 410 415
 Tyr Tyr Ser Gly Ser Gly Ile Trp Lys Asp Tyr Lys Leu Ala Phe Lys
 420 425 430
 Tyr Phe Tyr Leu Ala Ser Gln Ser Gly Gln Pro Leu Ala Ile Tyr Tyr
 435 440 445
 Leu Ala Lys Met Tyr Ala Thr Gly Thr Gly Val Val Arg Ser Cys Arg
 450 455 460
 Thr Ala Val Glu Lys Arg Leu Thr Phe Leu Lys Lys Arg Arg Cys Ile
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 Leu Leu Glu

<210> 11
 <211> 1731

<212> DNA

<213> Homo sapiens

<400> 11

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ggaattcaaa	ataaagatAT	cttgaagaga	aataagaatc	atttacaaaa	gcaagcagag	300
aaaaatttta	cagatgaagg	agaccagcta	tttaagatgg	gcatcaaggt	tctccagcag	360
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<210> 12

<211> 576

<212> PRT

<213> Homo sapiens

<400> 12

Met	Lys	Pro	Leu	Ser	Leu	Leu	Ile	Glu	Ile	Leu	Ile	Leu	Gly	Val	
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Thr	Ile	Lys	Thr	Ile	Lys	Ala	Glu	Glu	His	Asn	Lys	Arg	Gln	Lys	Glu
Arg	Asn	Val	Thr	Thr	Gln	Val	Ser	Val	Asn	Glu	Ile	Lys	Gln	Tyr	Leu
Ser	His	Ile	Leu	Glu	Gln	Arg	Thr	Ser	Ser	Asn	Val	Ile	Asn	Lys	Arg
Glu	Asn	Leu	Leu	Glu	Lys	Lys	Asn	Gln	Arg	Lys	Ile	Arg	Ile	Lys	
65															
Gly	Ile	Gln	Asn	Lys	Asp	Ile	Leu	Lys	Arg	Asn	Lys	Asn	His	Leu	Gln
85															
Lys	Gln	Ala	Glu	Lys	Asn	Phe	Thr	Asp	Glu	Gly	Asp	Gln	Leu	Phe	Lys
100															
Met	Gly	Ile	Lys	Val	Leu	Gln	Gln	Ser	Lys	Ser	Gln	Lys	Gln	Lys	Glu

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Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met	Gly Asn Leu Lys	
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Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe	Gly Asn Phe Gly Val	
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Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr	Glu Ser Leu Ala Lys	Glu
165	170	175
Gly Ser Cys Lys Ala Gln Asn Ala Leu	Gly Phe Leu Ser	Ser Tyr Gly
180	185	190
Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu	Ile Tyr Tyr Thr Phe	
195	200	205
Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met	Ile Leu Gly Tyr Arg	
210	215	220
Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys	Glu Val Ala Leu	Ser
225	230	235
Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp	Thr Phe Glu Lys	Ser
245	250	255
Glu Gly Val Pro Val Glu Lys Val Arg Leu	Thr Glu Arg Pro Glu Asn	
260	265	270
Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp	Ile Tyr Gln Tyr Tyr	
275	280	285
Lys Phe Leu Ala Glu Arg Gly Asp Val Gln	Ile Gln Val Ser Leu	Gly
290	295	300
Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp	Gln Asp Tyr Tyr Lys	
305	310	315
Ala Leu His Tyr Phe Leu Lys Ala Ala Lys	Ala Gly Ser Ala Asn	Ala
325	330	335
Met Ala Phe Ile Gly Lys Met Tyr Leu Glu	Gly Asn Ala Ala Val	Pro
340	345	350
Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe	Ser Met Ala Ala Ser	Lys
355	360	365
Gly Asn Ala Ile Gly Leu His Gly Leu	Gly Leu Tyr Phe His	Gly
370	375	380
Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala	Leu Lys Tyr Phe Gln	Lys
385	390	395
Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln	Phe Gln Leu Gly	Phe Met
405	410	415
Tyr Tyr Ser Gly Ser Gly Ile Trp Lys Asp	Tyr Lys Leu Ala Phe	Lys
420	425	430
Tyr Phe Tyr Leu Ala Ser Gln Ser Gly	Gln Pro Leu Ala Ile	Tyr Tyr
435	440	445
Leu Ala Lys Met Tyr Ala Thr Gly Thr	Gly Val Val Arg Ser	Cys Arg
450	455	460
Thr Ala Val Glu Lys Arg Leu Thr Phe	Leu Lys Arg Arg	Cys Ile
465	470	475
Gln Trp Arg Phe Ser Tyr Gly Ile Glu	Leu Pro Phe Lys Asp	Ile His
485	490	495
Leu Ala Arg Arg Leu Tyr Asp Met Ala Ala	Gln Thr Ser Pro Asp	Ala
500	505	510
His Ile Pro Val Leu Phe Ala Val Met Lys	Leu Glu Thr Thr His	Leu
515	520	525
Leu Arg Asp Ile Leu Phe Phe Asn Gln	Phe Thr Thr Arg Trp	Asn Trp
530	535	540
Leu Lys Leu Asp Asn Thr Ile Gly Pro His	Trp Asp Leu Phe Val	Ile
545	550	555
		560

Gly Leu Ile Val Pro Gly Leu Ile Leu Leu Leu Arg Asn His His Gly
 565 570 575

<210> 13

<211> 1728

<212> DNA

<213> Homo sapiens

<400> 13

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ggaattcaaa	ataaaagatAT	cttgaagaga	aataagaatc	atttacaaaa	gcaaggcagag	300
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<210> 14

<211> 575

<212> PRT

<213> Homo sapiens

<400> 14

Met	Lys	Pro	Leu	Ser	Leu	Leu	Ile	Glu	Ile	Leu	Ile	Leu	Gly	Val	
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Thr	Ile	Lys	Thr	Ile	Lys	Ala	Glu	Glu	His	Asn	Lys	Arg	Gln	Lys	Glu
						20		25			30				
Arg	Asn	Val	Thr	Thr	Gln	Val	Ser	Val	Asn	Glu	Ile	Lys	Gln	Tyr	Leu
						35		40			45				
Ser	His	Ile	Leu	Glu	Gln	Arg	Thr	Ser	Ser	Asn	Val	Ile	Asn	Lys	Arg
						50		55			60				
Glu	Asn	Leu	Leu	Glu	Lys	Lys	Asn	Gln	Arg	Lys	Ile	Arg	Ile	Lys	
							65		70		75			80	

Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
 85 90 95
 Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
 100 105 110
 Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
 115 120 125
 Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
 130 135 140
 Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
 145 150 155 160
 Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
 165 170 175
 Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
 180 185 190
 Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
 195 200 205
 Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
 210 215 220
 Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
 225 230 235 240
 Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
 245 250 255
 Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
 260 265 270
 Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
 275 280 285
 Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
 290 295 300
 Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
 305 310 315 320
 Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
 325 330 335
 Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
 340 345 350
 Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
 355 360 365
 Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
 370 375 380
 Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
 385 390 395 400
 Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
 405 410 415
 Tyr Tyr Ser Gly Ser Gly Ile Trp Lys Asp Tyr Lys Leu Ala Phe Lys
 420 425 430
 Tyr Phe Tyr Leu Ala Ser Gln Ser Gly Gln Pro Leu Ala Ile Tyr Tyr
 435 440 445
 Leu Ala Lys Met Tyr Ala Thr Gly Thr Gly Val Val Arg Ser Cys Arg
 450 455 460
 Thr Ala Val Glu Lys Arg Leu Thr Phe Leu Lys Lys Arg Arg Cys Ile
 465 470 475 480
 Gln Trp Arg Phe Ser Tyr Gly Ile Glu Leu Pro Phe Lys Asp Ile His
 485 490 495
 Leu Ala Arg Arg Leu Tyr Asp Met Ala Ala Gln Thr Ser Pro Asp Ala
 500 505 510
 His Ile Pro Val Leu Phe Ala Val Met Lys Leu Glu Thr Thr His Leu

515 520 525
Leu Arg Asp Ile Leu Phe Phe Asn Phe Thr Thr Arg Trp Asn Trp Leu
530 535 540
Lys Leu Asp Asn Thr Ile Gly Pro His Trp Asp Leu Phe Val Ile Gly
545 550 555 560
Leu Ile Val Pro Gly Leu Ile Leu Leu Arg Asn His His Gly
565 570 575